OM protein - nucleic search, using frame_plus_p2n model

Run on: January 17, 2003, 16:58:02 ; Search time 1852.4 Seconds
                                        (without alignments)
                                        122.402 Million cell updates/sec

Title: US-09-856-070-17
Perfect score: 69
Sequence: 1 EREFKFQMMFEKEEL 14

Scoring table. BLOSUM62
            Xgapop 10.0 , Xgapext   0.5
            Ygapop 10.0 , Ygapext   0.5
            Fgapop 6.0 , Fgapext   7.0
            Delop   6.0 , Delext   7.0

Searched.   16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 200000000000

Post-processing. Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame_plus_p2n model -DEV=xip
-Q=/cgr_2/USP90_sprot/USP9085070/pyrsnat_14012003_155844_1.rst/app_query fasta_1 1502
-DB-EST -QFMT=fastap -SUFFIX=rst -MINMAT=H=0.1 -L=PCL=0 -L=PEXT=0
-UNITS=bits -START=1 -END=-1 -MATPIX=blosum62 -TRANS=human40 cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN 15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAVSIZE=500 -MINLEN=0 -MAXLEN=20000000000
-USER=USP9085070 SCCN_1_3222 pranat_14012003_155844_1634 -NCPU=6 -COPU=1
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0 5 -FGAP0P=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0 5 -DELOP=6 -DELEXT=7

Database : EST   *
            1.   em_estba:*
            2.   em_esthum *
            3.   em_estin:*
            4.   em_estmu:*
            5.   em_estov:*
            6.   em_estpl:*
            7.   em_estro:*
            8.   em_htc:*
            9.   gb_estl:*
            10.   gb_est2:*
            11.   gb_htc:*
            12.   gb_est3:*
            13.   gb_est4:*
            14.   gb_est5:*
            15.   em_estiun:*
            16.   em_estrom:*
            17.   gb_gss *
            18.   em_gss_hum:*
            19.   em_gss_inv:*
            20.   em_gss_pln:*
            21.   em_gss_vrt:*
            22.   em_gss_fun:*
            23.   em_gss_mam:*
            24.   em_gss_mus:*
            25.   em_gss_other:*
            26.   em_gss_pro:*
            27.   em_gss_rod:*

Pred No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Pred	Description
1	69	100.0	214		BI052878	13	BI052878 RC5-GN228
2	69	100.0	214		BI054475	14	BI054475 RC5-GN028
3	69	100.0	215		BG754662	14	BG754662 RC5-GN028
4	69	100.0	234		BG754662	12	BG754662 692710194
5	69	100.0	245		BF844004	14	BE843004 MF4 ST024
6	69	100.0	275		BM844124	14	BM844124 K-EST0122
7	69	100.0	279		BF804323	14	BF804323 QV4-CI015
8	69	100.0	281		AW845219	10	AW845219 CM0-CT001
9	69	100.0	294		BI050028	13	BI050028 CM2-GN029
10	69	100.0	312		BM827086	14	BM827086 K FST0099
11	69	100.0	335		AI909763	9	AI909763 QV-BT233
12	69	100.0	458		BQ324947	14	BQ32383/ CMU-C1009
13	69	100.0	364		BQ308118	14	BQ308118 PM1-GN051
14	69	100.0	401		BQ318340	14	BQ318340 MR1-CT052
15	69	100.0	404		BM744771	14	BM744771 K-EST0018
16	69	100.0	413		BQ300862	14	BQ300862 MF4-KT004
17	69	100.0	432		BF804744	12	BF804744 MF1-CT052
18	69	100.0	437		BM844405	14	BM844405 K-EST0122
19	69	100.0	447		AW997331	10	AW997331 RC2-BN004
20	69	100.0	455		BM834336	14	BM834336 K-EST0109
21	69	100.0	460		BM846053	14	BM846053 K-EST0124
22	69	100.0	469		AI834242	9	AI834242 P20-HT001
23	69	100.0	484		AW845215	10	AW845215 CM0-CT001
24	69	100.0	484		BE314916	10	BE314916 601140093
25	69	100.0	484		BM834208	14	BM834208 K-EST0109
26	69	100.0	495		BI054723	14	BI054723 RC5-GN028
27	69	100.0	495		BM785233	14	BM785233 K-EST0089
28	69	100.0	507		BM840606	14	BM840606 K-EST0089
29	69	100.0	544		AW250260	10	AW250260 2821469.5
30	69	100.0	540		AI906462	14	AI906462 RC-BT108
31	69	100.0	540		BM746594	14	BM746594 K-EST0065
32	69	100.0	541		BM761260	14	BM761260 K-EST0042
33	69	100.0	548		BM788035	14	BM788035 K-EST0067
34	69	100.0	553		BM762412	14	BM762412 K-EST0044
35	69	100.0	556		BF946557	12	BF946557 MF4-GN015
36	69	100.0	564		BC746504	12	BC746504 602703802
37	69	100.0	572		BM744665	14	BM744665 K-EST0018
38	69	100.0	574		BM745443	10	BM745443 601174209
39	69	100.0	583		BM783500	14	BM783500 K-EST0061
40	69	100.0	590		BM783604	14	BM783604 K-EST0061
41	69	100.0	592		BM740878	14	BM740878 K-EST0013
42	69	100.0	593		BM838153	14	BM838153 K-EST0114
43	69	100.0	605		BE177808	10	BE177808 RC1-HT059
44	69	100.0	608		BI260897	13	BI260897 602702912
45	69	100.0	615		BM745140	14	BM745140 K-EST0063

ALIGNMENTS

RESULT 1
BI052878
LOCUS   BI052878   214 bp   mRNA   linear   EST 15-JUN-2001
DEFINITION RC5-GN0281-230101-021-F02 GN0281 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BI052878
VERSION   BI052878.1 GI:14460408
KEYWORDS   EST.
SOURCE   human.
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 214)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,

COMMENT

Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1-BC5&t2-BC5-GN0281-
010201-012-H01st3-2001-02-01st4-1)
Seq primer: puc 18 forward
High quality sequence stop: 214.

FEATURES   Location/qualifiers
source   1..214
                  /organism="Homo sapiens"
                  /db_xref="taxon:9606"
                  /clone_lib="GN0281"
                  /dev_stage="Adult"
                  /note="Organ: placenta normal; Vector: puc18; Site_1: SmaI
                  ; Site_2: SmaI; A mini library was made by cloning
                  products derived from ORESTES PCR (U.S. Letters Patent
                  application No. 196,716 - Ludwig Institute for Cancer
                  Research) profiles into the pUC 18 vector. Reverse
                  transcription of tissue mRNA and cDNA amplification were
                  performed under low stringency conditions."

BASE COUNT   68 a   36 c   88 g   22 t
ORIGIN

Alignment Scores:
Pred. No.:   0.121   Length: 214
Score: 69.00   Matches: 14
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 13   Indels: 0
DB: Gaps: 0

US-09-856-070-17 (1-14) x BIO54475 (1-214)

Qy   1 GluArgGluLysGluGlnMetMetArgGlyLysGluGluLeu 14
        ||||||||||||||||||||||||||||||||||||||||||
Db   23 GAGACAGAGAAAGACCCAGATGATGCGCGGGAAGAAGGAGTTG 64

RESULT 3
BQ367833/c
LOCUS   BQ367833   215 bp   mRNA   linear   EST 21-MAY-2002
DEFINITION   BC5-GN0281-150201-014-A02 GN0281 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BQ367833
VERSION   BQ367833.1   GI:21043334
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 215)
AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
               Nagai,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.F.,
               Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
               Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
               ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
               Simpson,A.J.
TITLE   Shotgun sequencing of the human transcriptome with ORF expressed
               sequence tags
JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE   20202663
COMMENT   Contact: Simpson A.J.G.
               Laboratory of Cancer Genetics
               Ludwig Institute for Cancer Research
               Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
               Brazil
               Tel: +55-11-2704922
               Fax: +55-11-2707001

Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACAGG(G). Size selected >500bp
for average insert size 1.8kb. Library constructed by Linq
Hsang in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC library."
Seq primer: puc 18 forward.

FEATURES
    source
        1..215
        /organism="Homo sapiens"
        /db_xref="taxon:9606"
        /clone_lib="GN0281"
        /dev_stage="Adult"
        /note="Organ: placenta_normal; Vector: puc18; Site_1: SmaI
        ; Site_2: SmaI; A mini library was made by cloning
        products derived from ORESTES PCR (U.S. Letters Patent
        application No. 196,716 - Ludwig Institute for Cancer
        Research) profiles into the puC 18 vector. Reverse
        transcription of tissue mRNA and cDNA amplification were
        performed under low stringency conditions."

BASE COUNT   22 a   91 c   34 g   68 t
ORIGIN

Alignment Scores:
Pred. No.:   0.121   Length: 215
Score: 69.00   Matches: 14
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 100.00%   Indels: 0
DB: Gaps: 0

US-09-856-070-17 (1-14) x HQ367833 (1-215)

Qy   1 GluArgGluLysGluGlnMetMetArgGluLysGluGluLeu 14
            |||||||||||||||||||||||||||||||||||||||||||
Db   193 GAGAGAGAAAGAGCAGATGATGCGAGAAAAGGAGGAGAGTTG 152

RESULT 4
HG754562
LOCUS   BG754562   234 bp   mRNA   linear   EST 15-MAY-2001
DEFINITION 602710194F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4846610 5',
            mRNA sequence.
ACCESSION   HG754562
VERSION   HG754562.1 GI:14065215
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 234)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/,
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1687 row: 1 column: 23
            High quality sequence stop: 234.

FEATURES
    source
        1..234
        /organism="Homo sapiens"
        /db_xref="taxon:9606"
        /clone="IMAGE:4846610"
        /clone_lib="NIH_MGC_48"
        /tissue_type="primary B-cells from tonsils (cell line)"
        /lab_host="DH10B (phage-resistant)"
        /note="Organ: B-cells; Vector: pCTB7, Site_1: XhoI,
        Site_2: EcoRI; cDNA made by oligo dT priming.

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?1-PCS&12-PCS-GN0281-
150201-01-A09&13-2001-02-15&t4-1)
Seq primer: puc 18 forward."

FEATURES
    source
        1..215
        /organism="Homo sapiens"
        /db_xref="taxon:9606"
        /clone_lib="GN0281"
        /dev_stage="Adult"

BASE COUNT   81 a   38 c   96 g   19 t
ORIGIN

Alignment Scores:
Pred. No.:   0.131   Length: 234
Score: 69.00   Matches: 14
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 100.00%   Indels: 0
Db: 12   Gaps: 0

US-09-856-070-17 (1-14) x HG754552 (1-234)

Qy   1 GluArgGluLysGluGlnMetMetArgGluLysGluGluLeu 14
            |||||||||||||||||||||||||||||||||||||||||||
Db   70 GAGAGAGAAAGAGCAGATGATGCGAGAAAAGGAGGAGAGTTG 111

RESULT 5
HG843004/C
LOCUS   BG843004   265 bp   mRNA   linear   EST 22-SEP-2000
DEFINITION MR4-ST0240-240700-012-h05 ST0240 Homo sapiens cDNA, mRNA sequence.
ACCESSION   HG843004
VERSION   HG843004.1 GI:10275382
KEYWORDS   EST.
SOURCE   Homo sapiens
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 265)
AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Kuia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J. Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
            Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
TITLE   Proc Natl Acad Sci U S A 97 (7), 3491-3496 (2000)
JOURNAL   20202663
MEDLINE   Contact: Simpson A.J.G.
COMMENT   Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509 010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?1-M&2-MR4-ST0240-240
            700-012-h05&t3-2000-07-24&t4-1)
            Seq primer: puc 18 forward
            High quality sequence start: 19
            High quality sequence stop: 265.

FEATURES
    source
        1..265
        /organism="Homo sapiens"
        /db_xref="taxon:9606"
        /clone_lib="ST0240"
        /dev_stage="Adult"
        /note="Organ: stomach; Vector: puc18; Site_1: SmaI
        site_2: SmaI; A mini-library was made by cloning products
        derived from ORESTES PCR (U.S. Letters Patent application
        No. 196,716 - Ludwig Institute for Cancer Research)
        profiles into the puC 18 vector. Reverse transcription of
        tissue mRNA and cDNA amplification were performed under

Alignment Scores:
Pred. No.:   0.154   Length: 275
Score: 69.00   Matches: 14
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: Indels: 0
DB: 14   Gaps: 0

US-09-856-070-17 (1-14) x BM844124 (1-275)

Qy   1 GluArgGluLysGlnIleMetMetArgGluLysGluGluLeu 14
          |||||||||||||||||||||||||||||||||||||||||
Db   15 GACAGAGAGAAAGAAAGAGAGTAGTAGTGCGGAGAGGAGAGTTG 56

RESULT 7
BM844323
LOCUS   BM844323   279 bp   mRNA   linear   EST 12-JAN-2001
DEFINITION QV4-CIO151 031100 513 105 CIO151 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BM844323
VERSION   BM844323.1   GI:12133312
KEYWORDS   EST.
SOURCE   human.
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 279)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., o'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE   Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
  COMMENT   Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509 010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV4&t2=CIO151-
            031100-513-105&t3=2000-11-03&t4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 279.
FEATURES   Location/Qualifiers
     source   1..279
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="CIO151"
                     /dev_stage="Adult"
                     /note="Organ: colon_ins; Vector: puc18; Site_1: Small;
                     Site_2: Small; A mini-library was made by cloning products
                     derived from ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 - Ludwig Institute for Cancer Research)
                     profiles into the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
BASE COUNT   88 a   53 c   111 g   27 t
ORIGIN

Alignment Scores:
Pred. No.:   0.156   Length: 279
Score: 69.00   Matches: 14
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: Indels: 0
DB: 12   Gaps: 0

BASE COUNT   40 a   88 c   58 g   79 t
ORIGIN

Alignment Scores:
Pred. No.:   0.148   Length: 265
Score: 69.00   Matches: 14
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: Indels: 0
DB: 12   Gaps: 0

US-09-856-070-17 (1-14) x BE843004 (1-265)

Qy   1 GluArgGluLysGlnIleMetMetArgGluLysGluGluLeu 14
          |||||||||||||||||||||||||||||||||||||||||
Db   58 GACAGAGAGAAAGAAAGAGAGTAGTAGTGCGGAGAGGAGAGTTG 17

RESULT 6
BM844124
LOCUS   BM844124   275 bp   mRNA   linear   EST 06-MAR-2002
DEFINITION K_EST0122163 S13KMS5 Homo sapiens cDNA clone S13KMS5-38-G03 5',
            mRNA sequence.
ACCESSION   BM844124
VERSION   BM844124.1   GI:14200533
KEYWORDS   EST.
SOURCE   human.
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 275)
  AUTHORS   Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
  TITLE   21C Frontier Korean EST Project 2001
  JOURNAL   Unpublished (2002)
  COMMENT   Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun dong Yuseong gu, Daejeon 305 333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 38 row: G column: 03
            High quality sequence stop: 275.
FEATURES   Location/Qualifiers
     source   1..275
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="S13KMS5-4R-G03"
                     /clone_lib="S13KMS5"
                     /tissue_type="myeloma"
                     /cell_line="KMS-5"
                     /lab_host="Top10F'"
                     /note="Vector: pCNS; Site_1: EcoRI; Site_2: NotI; The poly
                     (A)+ RNA was dephosphorylated with bacterial alkaline
                     phosphatase (BAP) and then decapped with tabacco acid
                     pyrophosphatase (TAP). The decapped intact mRNA was
                     ligated with DNA-RNA linker including EcoR I site by
                     treatment of T4 RNA ligase and the first strand cDNA was
                     synthesized from oligo dT-selected mRNA by priming with
                     dT-tailed vector. The dT-tailed vector was adjusted to
                     have about 60nt. The cDNA vector was circularized with E.
                     coli DNA ligase after digestion of EcoRI which site is
                     also included in vector. An RNA strand converted to a DNA
                     strand by Okayama-Berg method. The obtained cDNA vectors
                     were used for transformation of competent cells E. coli
                     Top10F' by electroporation method. The cDNA libraries
                     constructed by this method are full-length enriched cDNA
                     library."
BASE COUNT   81 a   48 c   117 g   29 t
ORIGIN

US-09-856-070-17 (1-14) x BF804323 (1-279)

```
Qy    1 GluArgLysGluGlnMetMetArgGluGluGluLeu 14
        ||||||||||||||||||||||||||||||||||||
Db   88 GAGAGAGAGAAAGAGCAGATGATGCGAGAAGAGGAGCTG 129
```

RESULT 8
AW845219
LOCUS   AW845219   281 bp   mRNA   linear   EST 19 MAY 2000
DEFINITION   CMC-CT0012 290644-017-a05 CT0012 Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW845219
VERSION   AW845219.1 GI:7940736
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 281)
AUTHORS   Dias Neto,E., Garcia Correa,P., Verjovski-Almeida,S., Briones,M.R.,
               Nagai,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.F.,
               Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
               Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,
               ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
               Simpson,A.J.
TITLE   Shotgun sequencing of the human transcriptome with ORF expressed
               sequence tags
JOURNAL   Proc. Natl. Acad. Sci. U.S.A 97 (7), 3491-3496 (2000).
MEDLINE   20202663
COMMENT   Contact: Simpson A.J.G.
               Laboratory of Cancer Genetics
               Ludwig Institute for Cancer Research
               Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
               Brazil
               Tel: +55-11-2704922
               Fax: +55-11-2707001
               Email: asimpson@ludwig.org.br
               This sequence was derived from the FAPESP/LICR Human Cancer Genome
               Project. This entry can be seen in the following URL
               (http://www.ludwig.org.br/scripts/gethtml2.pl?ut2=FMJ-Soul2-290
               699-017-a05&t3=1999-06-29&t4=1)
               Seq primer: puc 18 forward
               High quality sequence start: 10
               High quality sequence stop: 280
FEATURES   Location/Qualifiers
     source   1..281
               /organism="Homo sapiens"
               /db_xref="taxon:9606"
               /clone_lib="CT0012"
               /dev_stage="Adult"
               /note="Organ: colon; Vector: puc18, Site_1: Smal, Site_2:
               Smal; A mini-library was made by cloning products derived
               from ORESTES PCR (U.S. Letters Patent application No. 196
               ,716 - Ludwig Institute for Cancer Research) profiles
               into the pUC 18 vector. Reverse transcription of tissue
               mRNA and cDNA amplification were performed under low
               stringency conditions."

BASE COUNT   94 a   52 c   105 g   30 t
ORIGIN

Alignment Scores:
Pred. No.:   0.157
Score: 69.00
Percent Similarity: 100.00%   Length: 281
Host Local Similarity: 100.00%   Matches: 14
Query Match: 100.00%   Conservative: 0
DB: Mismatches: 0
                                             Indels: 0
                                             Gaps   0
```

US-09-856-070-17 (1-14) x AW845219 (1-281)

```
Qy    1 GluArgLysGluGlnMetMetArgGluGluGluLeu 14
        ||||||||||||||||||||||||||||||||||||
Db  143 GAGAGAGAGAAAGAGCAGATGATGCGAGAAGAGGAGCTG 184
```

RESULT 9
BI050028/c
LOCUS   BI050028   294 bp   mRNA   linear   EST 15 JUN 2001
DEFINITION   CM2-CN0294-020101-676-c09 CN0294 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BI050028
VERSION   BI050028.1 GI:14457558
KEYWORDS   EST.
SOURCE   human.
ORGANISM   Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 294)
AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
               Nagai,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.F.,
               Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
               Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
               ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
               Simpson,A.J.
TITLE   Shotgun sequencing of the human transcriptome with ORF expressed
               sequence tags
JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE   20202663
COMMENT   Contact: Simpson A.J.G.
               Laboratory of Cancer Genetics
               Ludwig Institute for Cancer Research
               Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
               Brazil
               Tel: +55-11-2704922
               Fax: +55-11-2707001
               Email: asimpson@ludwig.org.br
               This sequence was derived from the FAPESP/LICR Human Cancer Genome
               Project. This entry can be seen in the following URL
               (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=CN0294-CM2-CN0294-
               020101-676-c09&t3=2001-01-02&t4=1)
               Seq primer: puc 18 forward
               High quality sequence start: 17
               High quality sequence stop: 294.
FEATURES   Location/Qualifiers
     source   1..294
               /organism="Homo sapiens"
               /db_xref="taxon:9606"
               /clone_lib="CN0294"
               /dev_stage="Adult"
               /note="Organ: placenta_normal; Vector: puc18; Site_1: Smal
               ; Site_2: Smal; A mini-library was made by cloning
               products derived from ORESTES PCR (U.S. Letters Patent
               application No. 196,716 - Ludwig Institute for Cancer
               Research) profiles into the pUC 18 vector. Reverse
               transcription of tissue mRNA and cDNA amplification were
               performed under low stringency conditions."

BASE COUNT   34 a   114 c   56 g   90 t
ORIGIN

Alignment Scores:
Pred. No.:   0.154
Score: 69.00
Percent Similarity: 100.00%   Length: 294
Host Local Similarity: 100.00%   Matches: 14
Query Match: Conservative: 0
DB: Mismatches: 0
                                             Indels: 0
                                             Gaps: 0
```

US-09-856-070-17 (1-14) x BI050028 (1-294)

```
Qy    1 GluArgLysGluGlnMetArgGluGluGluLeu 14
        |||||||||||||||||||||||||||||||
Db  246 GAGAGAGAGAAGAGATAGAAGCGAGAAGAGGAGTTG 205
```

RESULT 10
BM827086
LOCUS   BM827086   312 bp   mRNA   linear   EST 06 MAR 2002
DEFINITION   K-EST0099421 S9SNH601 Homo sapiens cDNA clone S9SNH601 44-G09 5',
               mRNA sequence.
```

ACCESSION   BM827086
VERSION     BM827086.1  GI:19184495
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 312)
  AUTHORS   Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
  TITLE     21C Frontier Korean EST Project 2001
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 44  row: C  column: 09
            High quality sequence stop: 312.
FEATURES             Location/Qualifiers
     source          1..312
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="S4SNU601-44-C09"
                     /clone_lib="S4SNU601"
                     /sex="M"
                     /tissue_type="Ascites"
                     /cell_type="Epithelial"
                     /cell_line="SNU-601"
                     /lab_host="Top10F'"
                     /note="organ: Stomach; Vector: pME18S-FL3; Site_1: XhoI;
                     Site_2: XhoI. The poly (A)+ RNA was dephosphorylated with
                     bacterial alkaline phosphatase (BAP) and then decapped
                     with tabacco acid pyrophosphatase (TAP). The decapped
                     intact mRNA was ligated with DNA-RNA linker including SfiI
                     site by treatment of T4 RNA ligase and the first strand
                     cDNA was synthesized with Superscript II using SfiI
                     oligo-dT primer. After first strand synthesis, RNA was
                     degraded by NaOH treatment and cDNA was amplified by PCR
                     reaction. The PCR products were digested with SfiI and
                     cloned into braIII-digested pME18S-FL3 vector. The
                     obtained cDNA vectors were used for transformation of
                     competent cells E. coli Top10F' by electroporation method
                     the cDNA libraries constructed by this method are
                     full-length enriched cDNA library."
BASE COUNT   108 a   60 c   110 g   34 t
ORIGIN

Alignment Scores:
Prod. No.:                          312
Score:                    0.174     Matches:          14
Percent Similarity:     69.00       Conservative:      0
Best Local Similarity:  100.00%     Mismatches:        0
Query Match:            100.00%     Indels:            0
DB:                         14      Gaps:              0

US-09-856-070-17 (1-14) x BM827086 (1-312)

Qy     1  GluArgGluLysGluGlnMetMetArgGluLysGluGluLeu 14
          ||||||||||||||||||||||||||||||||||||||||||
Db   182  GAGAGAGAAAGAGCAGATGATGCGCGAGAAGGAGGAGTTG 223

RESULT 11
AI909763
LOCUS       AI909763     335 bp     mRNA    linear   EST 30-MAR-2000
DEFINITION  QV-BT223-220499-046-h05 BT223 Homo sapiens cDNA, mRNA sequence.
ACCESSION   AI909763
VERSION     AI909763.1  GI:5650044?
KEYWORDS    EST.
SOURCE      human.

---

ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 335)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,
            M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/seq/gct.html ?LPtl-QV&t2-QV-BT223-036.html
            &t3-22049&t4-1)
            Seq primer: puc 18 forward.
FEATURES             Location/Qualifiers
     source          1..335
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="BT223"
                     /sex="female"
                     /dev_stage="Adult"
                     /note="organ: breast; vector: puc18; Site_1: SmaI; Site_2:
                     SmaI. A mini-library was made by cloning products derived
                     from ORESTES PCR (U.S. Letters Patent application No. 196
                     ,716 - Ludwig Institute for Cancer Research) profiles
                     into the pUC 18 vector. Reverse transcription of tissue
                     mRNA and cDNA amplification were performed under low
                     stringency conditions."
BASE COUNT   103 a   65 c   128 g   39 t
ORIGIN

Alignment Scores:
Prod. No.:                          335
Score:                    0.185     Matches:          14
Percent Similarity:     69.00       Conservative:      0
Best Local Similarity:  100.00%     Mismatches:        0
Query Match:            100.00%     Indels:            0
DB:                          9      Gaps:              0

US-09-856-070-17 (1-14) x AI909763 (1-335)

Qy     1  GluArgGluLysGluGlnMetMetArgGluLysGluGluLeu 14
          ||||||||||||||||||||||||||||||||||||||||||
Db   143  GAGAGAGAAAGAGCAGATGATGCGCGAGAAGGAGGAGTTG 184

RESULT 12
BQ323837
LOCUS       BQ323837     358 bp     mRNA    linear   EST 17-MAY-2002
DEFINITION  CM0-C0095-101000-648-b05 CI0095 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BQ323837
VERSION     BQ323837.1  GI:20935634
KEYWORDS    EST.
SOURCE      human.
            Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 358)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,

TITLE       Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
            Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
JOURNAL     Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE     20202663
COMMENT     Contact: Simpson A.J.G
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: ajsimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL.
            (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM0&t2=CM0-CI0095-
            301000-648-b05&t3=2000-10-30&t4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 2.
FEATURES    Location/Qualifiers
     source 1..358
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone_lib="CI0095"
            /dev_stage="Adult"
            /note="Organ: colon_lts, Vector: puc18, Site_1: SmaI,
            Site_2: SmaI. A mini library was made by cloning products
            derived from ORESTES PCR (U.S. Letters Patent application
            No.196,716 - Ludwig Institute for Cancer Research)
            profiles into the puc 18 vector Reverse transcription of
            tissue mRNA and cDNA amplification were performed under
            low stringency conditions."
BASE COUNT  112 a      74 c     130 g      42 t
ORIGIN

Alignment Scores:
Pred. No.:              0.199
Score:                  69.00
Percent Similarity:     100.00%
Best Local Similarity:  100.00%
Query Match:            14
DB:

US-09-856-070-17 (1-14) x BQ323837 (1-358)

Qy     1 GluArgGluLysGluGlnMetMetArgGluLysGluGluLeu 14
         ||||||||||||||||||||||||||||||||||||||||||
Db   195 GAGAGAGAGAAAGAGCAGATGATGCGCGAGAAGGAGGAGTTG 236

RESULT 13
BQ368118
LOCUS       BQ368118           364 bp     mRNA    linear   EST 21-MAY-2002
DEFINITION  PM3-GN0516-001501-010-d10 GN0516 Homo sapiens cDNA, mRNA sequence
ACCESSION   BQ368118
VERSION     BQ368118.1  GI:21043632
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 364)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663

COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: ajsimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL.
            (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM3&t2=PM3-GN0516-
            090501-010-d10&t3=2001-05-09&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 11
            High quality sequence stop: 348
FEATURES    Location/Qualifiers
     source 1..364
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone_lib="GN0516"
            /dev_stage="Adult"
            /note="Organ: placenta_normal, Vector: puc18, Site_1: SmaI
            , Site_2: SmaI. A mini library was made by cloning
            products derived from ORESTES PCR (U.S. Letters Patent
            application No.196,716 - Ludwig Institute for Cancer
            Research) profiles into the puc 18 vector Reverse
            transcription of tissue mRNA and cDNA amplification were
            performed under low stringency conditions."
BASE COUNT  112 a      54 c     146 g      42 t
ORIGIN

Alignment Scores:
Pred. No.:              0.202
Score:                  69.00
Percent Similarity:     100.00%
Best Local Similarity:  100.00%
Query Match:            14
DB:

US-09-856-070-17 (1-14) x BQ368118 (1-364)

Qy     1 GluArgGluLysGluGlnMetMetArgGluLysGluGluLeu 14
         ||||||||||||||||||||||||||||||||||||||||||
Db    89 GAGAGAGAGAAAGAGCAGATGATGCGCGAGAAGGAGGAGTTG 130

RESULT 14
BQ318340/c
LOCUS       BQ318340           401 bp     mRNA    linear   EST 17-MAY-2002
DEFINITION  MF1-CT0529-140000-002-a12 CT0529 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BQ318340
VERSION     BQ318340.1  GI:20924109
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 401)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922

```
        Fax: +55 11 2707001
        Email: asimpson@ludwig.org.br
        This sequence was derived from the FAPESP/LICR Human Cancer Genome
        Project. This entry can be seen in the following URL
        (http://www.ludwig.org.br/scripts/gethtml2.pl?ti MP:5.4-MRI C795-9-
        140900-0002-3124+3-2000-09-14+t4-1)
        Seq primer: puc18 forward
        High quality sequence start: 2
        High quality sequence stop: 401.
FEATURES         Location/Qualifiers
     source    1..401
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone_lib="C10529"
                /dev_stage="Adult"
                /note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
                SmaI; A mini-library was made by cloning products derived
                from ORESTES PCR (U.S. Letters Patent application No. 196
                ,716 - Ludwig Institute for Cancer Research) profiles
                into the puC 18 vector. Reverse transcription of tissue
                mRNA and cDNA amplification were performed under low
                stringency conditions."
BASE COUNT        56 a     144 c      73 g     128 t
ORIGIN

Alignment Scores:
Pred. No.:                          0.222        Length:         401
Score:                             69.00         Matches:         14
Percent Similarity:               100.00%        Conservative:     0
Best Local Similarity:            100.00%        Mismatches:       0
Query Match:                      100.00%        Indels:           0
Db:                                  14          Gaps:             0

US-09-856-070-17 (1-14) x BQ418340 (1-401)

Qy    1 GluArgGluLysGluGlnMetMetArgGluLysGluGluLen 14
        ||||||||||||||||||||||||||||||||||||||||||
Db  285 CAGAGACAGAAGAAGATGATGCGGGAGAAGGAGGAGTTG 244


RESULT 15
LOCUS       BM744771
LOCUS       BM744771
DEFINITION  K-KST0018496 S4SNU1 Homo sapiens cDNA clone S4SNU1-18-D12 5', mRNA
            sequence.
ACCESSION   BM744771
VERSION     BM744771.1  GI:19066100
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 404)
AUTHORS     Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
TITLE       21C Frontier Korean EST Project 2001
JOURNAL     Unpublished (2002)
COMMENT     Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun dong Yuseong gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yonusun@mail.kribb.re.kr
            Plate: 18 row: D column: 12
            High quality sequence stop: 404.
FEATURES         Location/Qualifiers
     source    1..404
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="S4SNU1-18-D12"
                /clone_lib="S4SNU1"
                /sex="M"
```

```
                /tissue_type="Stomach"
                /cell_type="Lymphoblast-like"
                /cell_line="SNU-1"
                /lab_host="Top10F'"
                /note="Organ: Stomach. Vector: pT7T8RP1; Site_1: EcoRI;
                Site_2: NotI. The poly (A)+ RNA was dephosphorylated with
                bacterial alkaline phosphatase (BAP) and then decapped
                with tobacco acid pyrophosphatase (TAP). The decapped
                intact mRNA was ligated with DNA RNA linker including EcoR
                I site by treatment of T4 RNA ligase and the first strand
                cDNA was synthesized from oligo dT-selected mRNA by
                priming with dt-tailed vector. The dt-tailed vector was
                adjusted to have about 60nt. The cDNA vector was
                circularized with E. coli DNA ligase after digestion of
                EcoRI which site is also included in vector. An RNA strand
                converted to a DNA strand by Okayama Berg method. The
                obtained cDNA vectors were used for transformation of
                competent cells E. coli Top10F' by electroporation method.
                The cDNA libraries constructed by this method are
                full-length enriched cDNA library."
BASE COUNT       127 a      83 c     141 g      53 t
ORIGIN

Alignment Scores:
Pred. No.:                          0.224        Length:         404
Score:                             69.00         Matches:         14
Percent Similarity:               100.00%        Conservative:     0
Best Local Similarity:            100.00%        Mismatches:       0
Query Match:                      100.00%        Indels:           0
Db:                                  14          Gaps:             0

US-09-856-070-17 (1-14) x BM744771 (1-404)

Qy    1 GluArgGluLysGluGlnMetMetArgGluLysGluGluLen 14
        ||||||||||||||||||||||||||||||||||||||||||
Db  240 CAGAGACAGAAGAACAGAAGATGATGCGGGAGAAGGAGGAGTTG 281


Search completed: January 15, 2003, 21:37:02
Job time : 1856.4 secs
```